



PCT10

ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/070,798

DATE: 03/21/2002

TIME: 15:49:58

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\03212002\J070798.raw

#1/R20  
Seg

3 <110> APPLICANT: Brett P. Monia  
4 Lex M. Cowser  
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PI3 KINASE P110 BETA EXPRESSION  
8 <130> FILE REFERENCE: RTS-0075  
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/070,798  
C--> 10 <141> CURRENT FILING DATE: 2002-03-08  
10 <160> NUMBER OF SEQ ID NOS: 47  
12 <210> SEQ ID NO: 1  
13 <211> LENGTH: 3213  
14 <212> TYPE: DNA  
15 <213> ORGANISM: Homo sapiens  
17 <220> FEATURE:  
18 <221> NAME/KEY: CDS  
19 <222> LOCATION: (1)..(3213)  
21 <400> SEQUENCE: 1  
22 atg tgc ttc agt ttc ata atg cct cct gct atg gca gac atc ctt gac 48  
23 Met Cys Phe Ser Phe Ile Met Pro Pro Ala Met Ala Asp Ile Leu Asp  
24 1 5 10 15  
26 atc tgg gcg gtg gat tca cag ata gca tct gat ggc tcc ata cct gtg 96  
27 Ile Trp Ala Val Asp Ser Gln Ile Ala Ser Asp Gly Ser Ile Pro Val  
28 20 25 30  
30 gat ttc ctt ttg ccc act ggg att tat atc cag ttg gag gta cct cgg 144  
31 Asp Phe Leu Leu Pro Thr Gly Ile Tyr Ile Gln Leu Glu Val Pro Arg  
32 35 40 45  
34 gaa gct acc att tct tat att aag cag atg tta tgg aag caa gtt cac 192  
35 Glu Ala Thr Ile Ser Tyr Ile Lys Gln Met Leu Trp Lys Gln Val His  
36 50 55 60  
38 aat tac cca atg ttc aac ctc ctt atg gat att gac tcc tat atg ttt 240  
39 Asn Tyr Pro Met Phe Asn Leu Leu Met Asp Ile Asp Ser Tyr Met Phe  
40 65 70 75 80  
42 gca tgt gtg aat cag act gct gta tat gag gag ctt gaa gat gaa aca 288  
43 Ala Cys Val Asn Gln Thr Ala Val Tyr Glu Glu Leu Glu Asp Glu Thr  
44 85 90 95  
46 cga aga ctc tgt gat gtc aga cct ttt ctt cca gtt ctc aaa tta gtg 336  
47 Arg Arg Leu Cys Asp Val Arg Pro Phe Leu Pro Val Leu Lys Leu Val  
48 100 105 110  
50 aca aga agt tgt gac cca ggg gaa aaa tta gac tca aaa att gga gtc 384  
51 Thr Arg Ser Cys Asp Pro Gly Glu Lys Leu Asp Ser Lys Ile Gly Val  
52 115 120 125  
54 ctt ata gga aaa ggt ctg cat gaa ttt gat tcc ttg aag gat cct gaa 432  
55 Leu Ile Gly Lys Gly Leu His Glu Phe Asp Ser Leu Lys Asp Pro Glu  
56 130 135 140  
58 gta aat gaa ttt cga aga aaa atg cgc aaa ttc agc gag gaa aaa atc 480

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59	Val	Asn	Glu	Phe	Arg	Arg	Lys	Met	Arg	Lys	Phe	Ser	Glu	Glu	Lys	Ile	
60	145						150				155					160	
63	ctg	tca	ctt	gtg	gga	ttg	tct	tgg	atg	gac	tgg	cta	aaa	caa	aca	tat	528
64	Leu	Ser	Leu	Val	Gly	Leu	Ser	Trp	Met	Asp	Trp	Leu	Lys	Gln	Thr	Tyr	
65					165					170					175		
67	cca	cca	gag	cat	gaa	cca	tcc	atc	cct	gaa	aac	tta	gaa	gat	aaa	ctt	576
68	Pro	Pro	Glu	His	Glu	Pro	Ser	Ile	Pro	Glu	Asn	Leu	Glu	Asp	Lys	Leu	
69				180					185					190			
71	tat	ggg	gga	aag	ctc	atc	gta	gct	gtt	cat	ttt	gaa	aac	tgc	cag	gac	624
72	Tyr	Gly	Gly	Lys	Leu	Ile	Val	Ala	Val	His	Phe	Glu	Asn	Cys	Gln	Asp	
73		195						200					205				
75	gtg	ttt	agc	ttt	caa	gtg	tct	cct	aat	atg	aat	cct	atc	aaa	gta	aat	672
76	Val	Phe	Ser	Phe	Gln	Val	Ser	Pro	Asn	Met	Asn	Pro	Ile	Lys	Val	Asn	
77		210					215					220					
79	gaa	ttg	gca	atc	caa	aaa	cgt	ttg	act	att	cat	ggg	aag	gaa	gat	gaa	720
80	Glu	Leu	Ala	Ile	Gln	Lys	Arg	Leu	Thr	Ile	His	Gly	Lys	Glu	Asp	Glu	
81	225				230						235				240		
83	gtt	agc	ccc	tat	gat	tat	gtg	ttg	caa	gtc	agc	ggg	aga	gta	gaa	tat	768
84	Val	Ser	Pro	Tyr	Asp	Tyr	Val	Leu	Gln	Val	Ser	Gly	Arg	Val	Glu	Tyr	
85				245					250					255			
87	gtt	ttt	ggt	gat	cat	cca	cta	att	cag	ttc	cag	tat	atc	cgg	aac	tgt	816
88	Val	Phe	Gly	Asp	His	Pro	Leu	Ile	Gln	Phe	Gln	Tyr	Ile	Arg	Asn	Cys	
89			260						265				270				
91	gtg	atg	aac	aga	gcc	ctg	ccc	cat	ttt	ata	ctt	gtg	gaa	tgc	tgc	aag	864
92	Val	Met	Asn	Arg	Ala	Leu	Pro	His	Phe	Ile	Leu	Val	Glu	Cys	Cys	Lys	
93		275					280					285					
95	atc	aag	aaa	atg	tat	gaa	caa	gaa	atg	att	gcc	ata	gag	gct	gcc	ata	912
96	Ile	Lys	Lys	Met	Tyr	Glu	Gln	Glu	Met	Ile	Ala	Ile	Glu	Ala	Ala	Ile	
97		290				295					300						
99	aat	cga	aat	tca	tct	aat	ctt	cct	ctt	cca	tta	cca	cca	aag	aaa	aca	960
100	Asn	Arg	Asn	Ser	Ser	Asn	Leu	Pro	Leu	Pro	Leu	Pro	Pro	Lys	Lys	Thr	
101	305					310					315				320		
103	cga	att	att	tct	cat	gtt	tgg	gaa	aat	aac	aac	cct	ttc	caa	att	gtc	1008
104	Arg	Ile	Ile	Ser	His	Val	Trp	Glu	Asn	Asn	Asn	Pro	Phe	Gln	Ile	Val	
105				325					330				335				
107	ttg	gtt	aag	gga	aat	aaa	ctt	aac	aca	gag	gaa	act	gta	aaa	gtt	cat	1056
108	Leu	Val	Lys	Gly	Asn	Lys	Leu	Asn	Thr	Glu	Glu	Thr	Val	Lys	Val	His	
109			340						345				350				
111	gtc	agg	gct	ggt	ctt	ttt	cat	ggt	act	gag	ctc	ctg	tgt	aaa	acc	atc	1104
112	Val	Arg	Ala	Gly	Leu	Phe	His	Gly	Thr	Glu	Leu	Leu	Cys	Lys	Thr	Ile	
113		355					360					365					
115	gta	agc	tca	gag	gta	tca	ggg	aaa	aat	gat	cat	att	tgg	aat	gaa	cca	1152
116	Val	Ser	Ser	Glu	Val	Ser	Gly	Lys	Asn	Asp	His	Ile	Trp	Asn	Glu	Pro	
117		370					375				380						
119	ctg	gaa	ttt	gat	att	aat	att	tgt	gac	tta	cca	aga	atg	gct	cga	tta	1200
120	Leu	Glu	Phe	Asp	Ile	Asn	Ile	Cys	Asp	Leu	Pro	Arg	Met	Ala	Arg	Leu	
121	385				390					395				400			
123	tgt	ttt	gct	gtt	tat	gca	gtt	ttg	gat	aaa	gta	aaa	acg	aag	aaa	tca	1248
125	Cys	Phe	Ala	Val	Tyr	Ala	Val	Leu	Asp	Lys	Val	Lys	Thr	Lys	Lys	Ser	

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126					405				410					415			
128	acg	aaa	act	att	aat	ccc	tct	aaa	tat	cag	acc	atc	agg	aaa	gct	gga	1296
129	Thr	Lys	Thr	Ile	Asn	Pro	Ser	Lys	Tyr	Gln	Thr	Ile	Arg	Lys	Ala	Gly	
130					420				425					430			
132	aaa	gtg	cat	tat	cct	gta	gcg	tggt	gta	aat	acg	atg	gtt	ttt	gac	ttt	1344
133	Lys	Val	His	Tyr	Pro	Val	Ala	Trp	Val	Asn	Thr	Met	Val	Phe	Asp	Phe	
134					435				440					445			
136	aaa	gga	caa	ttg	aga	act	gga	gac	ata	ata	tta	cac	agc	tggt	tct	tca	1392
137	Lys	Gly	Gln	Leu	Arg	Thr	Gly	Asp	Ile	Ile	Leu	His	Ser	Trp	Ser	Ser	
138					450				455					460			
140	ttt	cct	gat	gaa	ctc	gaa	gaa	atg	ttg	aat	cca	atg	gga	act	gtt	caa	1440
141	Phe	Pro	Asp	Glu	Leu	Glu	Glu	Met	Leu	Asn	Pro	Met	Gly	Thr	Val	Gln	
142	465								470					475		480	
144	aca	aat	cca	tat	act	gaa	aat	gca	aca	gct	ttg	cat	gtt	aaa	ttt	cca	1488
145	Thr	Asn	Pro	Tyr	Thr	Glu	Asn	Ala	Thr	Ala	Leu	His	Val	Lys	Phe	Pro	
146					485				490					495			
148	gag	aat	aaa	aaa	caa	cct	tat	tat	tac	cct	ccc	ttc	gat	aag	att	att	1536
149	Glu	Asn	Lys	Lys	Gln	Pro	Tyr	Tyr	Tyr	Pro	Pro	Phe	Asp	Lys	Ile	Ile	
150					500				505					510			
152	gaa	aag	gca	gct	gag	att	gca	agc	agt	gat	agt	gct	aat	gtg	tca	agt	1584
153	Glu	Lys	Ala	Ala	Glu	Ile	Ala	Ser	Ser	Asp	Ser	Ala	Asn	Val	Ser	Ser	
154					515				520					525			
156	cga	ggt	gga	aaa	aag	ttt	ctt	cct	gta	ttg	aaa	gaa	atc	ttg	gac	agg	1632
157	Arg	Gly	Gly	Lys	Lys	Phe	Leu	Pro	Val	Leu	Lys	Glu	Ile	Leu	Asp	Arg	
158					530				535					540			
160	gat	ccc	ttg	tct	caa	ctg	tgt	gaa	aat	gaa	atg	gat	ctt	att	tggt	act	1680
161	Asp	Pro	Leu	Ser	Gln	Leu	Cys	Glu	Asn	Glu	Met	Asp	Leu	Ile	Trp	Thr	
162	545					550					555				560		
164	ttg	cga	caa	gac	tgc	cga	gag	att	ttc	cca	caa	tca	ctg	cca	aaa	tta	1728
165	Leu	Arg	Gln	Asp	Cys	Arg	Glu	Ile	Phe	Pro	Gln	Ser	Leu	Pro	Lys	Leu	
166					565					570					575		
168	ctg	ctg	tca	atc	aag	tggt	aat	aaa	ctt	gag	gat	gtt	gct	cag	ctt	cag	1776
169	Leu	Leu	Ser	Ile	Lys	Trp	Asn	Lys	Leu	Glu	Asp	Val	Ala	Gln	Leu	Gln	
170					580				585					590			
172	gcg	ctg	ctt	cag	att	tggt	cct	aaa	ctg	ccc	ccc	cgg	gag	gcc	cta	gag	1824
173	Ala	Leu	Leu	Gln	Ile	Trp	Pro	Lys	Leu	Pro	Pro	Arg	Glu	Ala	Leu	Glu	
174					595				600					605			
176	ctt	ctg	gat	ttc	aac	tat	cca	gac	cag	tac	gtt	cga	gaa	tat	gct	gta	1872
177	Leu	Leu	Asp	Phe	Asn	Tyr	Pro	Asp	Gln	Tyr	Val	Arg	Glu	Tyr	Ala	Val	
178					610				615					620			
180	ggc	tggt	ctg	cga	cag	atg	agt	gat	gaa	gaa	ctt	tct	caa	tat	ctt	tta	1920
181	Gly	Cys	Leu	Arg	Gln	Met	Ser	Asp	Glu	Glu	Leu	Ser	Gln	Tyr	Leu	Leu	
182	625					630					635				640		
184	caa	ctg	gtg	caa	gtg	tta	aaa	tat	gag	cct	ttt	ctt	gat	tgt	gcc	ctc	1968
185	Gln	Leu	Val	Gln	Val	Leu	Lys	Tyr	Glu	Pro	Phe	Leu	Asp	Cys	Ala	Leu	
187					645					650				655			
189	tct	aga	ttc	cta	tta	gaa	aga	gca	ctt	ggt	aat	cgg	agg	ata	gggt	cag	2016
190	Ser	Arg	Phe	Leu	Leu	Glu	Arg	Ala	Leu	Gly	Asn	Arg	Arg	Ile	Gly	Gln	
191					660				665					670			

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193	ttt	cta	ttt	tgg	cat	ctt	agg	tca	gaa	gtg	cac	att	cct	gct	gtc	tca	2064
194	Phe	Leu	Phe	Trp	His	Leu	Arg	Ser	Glu	Val	His	Ile	Pro	Ala	Val	Ser	
195			675						680				685				
197	gta	caa	ttt	ggg	gtc	atc	ctt	gaa	gca	tac	tgc	cgg	gga	agt	gtg	ggg	2112
198	Val	Gln	Phe	Gly	Val	Ile	Leu	Glu	Ala	Tyr	Cys	Arg	Gly	Ser	Val	Gly	
199		690					695					700					
201	cac	atg	aaa	gtg	ctt	tct	aag	cag	ggt	gaa	gca	ctc	aat	aag	tta	aaa	2160
202	His	Met	Lys	Val	Leu	Ser	Lys	Gln	Val	Glu	Ala	Leu	Asn	Lys	Leu	Lys	
203	705					710					715					720	
205	act	tta	aat	agt	tta	atc	aaa	ctg	aat	gcc	gtg	aag	tta	aac	aga	gcc	2208
206	Thr	Leu	Asn	Ser	Leu	Ile	Lys	Leu	Asn	Ala	Val	Lys	Leu	Asn	Arg	Ala	
207						725					730					735	
209	aaa	ggg	aag	gag	gcc	atg	cat	acc	tgt	tta	aaa	cag	agt	gct	tac	cgg	2256
210	Lys	Gly	Lys	Glu	Ala	Met	His	Thr	Cys	Leu	Lys	Gln	Ser	Ala	Tyr	Arg	
211			740						745				750				
213	gaa	gcc	ctc	tct	gac	ctg	cag	tca	ccc	ctg	aac	cca	tgt	gtt	atc	ctc	2304
214	Glu	Ala	Leu	Ser	Asp	Leu	Gln	Ser	Pro	Leu	Asn	Pro	Cys	Val	Ile	Leu	
215			755						760				765				
217	tca	gaa	ctc	tat	gtt	gaa	aag	tgc	aaa	tac	atg	gat	tcc	aaa	atg	aag	2352
218	Ser	Glu	Leu	Tyr	Val	Glu	Lys	Cys	Lys	Tyr	Met	Asp	Ser	Lys	Met	Lys	
219		770					775					780					
221	cct	ttg	tgg	ctg	gta	tac	aat	aac	aag	gta	ttt	ggg	gag	gat	tca	gtt	2400
222	Pro	Leu	Trp	Leu	Val	Tyr	Asn	Asn	Lys	Val	Phe	Gly	Glu	Asp	Ser	Val	
223	785					790					795					800	
225	gga	gtg	att	ttt	aaa	aat	ggg	gat	gat	tta	cga	cag	gat	atg	ttg	aca	2448
226	Gly	Val	Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr	
227					805					810						815	
229	ctc	caa	atg	ttg	cgc	ttg	atg	gat	tta	ctc	tgg	aaa	gaa	gct	ggg	ttg	2496
230	Leu	Gln	Met	Leu	Arg	Leu	Met	Asp	Leu	Leu	Trp	Lys	Glu	Ala	Gly	Leu	
231					820					825						830	
233	gat	ctt	cgg	atg	ttg	cct	tat	ggc	tgt	tta	gca	aca	gga	gat	cgc	tct	2544
234	Asp	Leu	Arg	Met	Leu	Pro	Tyr	Gly	Cys	Leu	Ala	Thr	Gly	Asp	Arg	Ser	
235			835						840				845				
237	ggc	ctc	att	gaa	gtt	gtg	agc	acc	tct	gaa	aca	att	gct	gac	att	cag	2592
238	Gly	Leu	Ile	Glu	Val	Val	Ser	Thr	Ser	Glu	Thr	Ile	Ala	Asp	Ile	Gln	
239		850					855					860					
241	ctg	aac	agt	agc	aat	gtg	gct	gct	gca	gca	gcc	ttc	aac	aaa	gat	gcc	2640
242	Leu	Asn	Ser	Ser	Asn	Val	Ala	Ala	Ala	Ala	Ala	Phe	Asn	Lys	Asp	Ala	
243	865					870					875					880	
245	ctt	ctg	aac	tgg	ctt	aaa	gaa	tac	aac	tct	ggg	gat	gac	ctg	gac	cga	2688
246	Leu	Leu	Asn	Trp	Leu	Lys	Glu	Tyr	Asn	Ser	Gly	Asp	Asp	Leu	Asp	Arg	
247					885					890						895	
249	gcc	att	gag	gaa	ttt	aca	ctg	tcc	tgt	gct	ggc	tac	tgt	gta	gct	tct	2736
250	Ala	Ile	Glu	Glu	Phe	Thr	Leu	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Ser	
251			900						905					910			
253	tat	gtc	ctt	ggg	att	ggg	gac	aga	cat	agt	gac	aac	atc	atg	gtc	aaa	2784
254	Tyr	Val	Leu	Gly	Ile	Gly	Asp	Arg	His	Ser	Asp	Asn	Ile	Met	Val	Lys	
255			915						920					925			
257	aaa	act	ggc	cag	ctc	ttc	cac	att	gac	ttt	gga	cat	att	ctt	gga	aat	2832

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258 Lys Thr Gly Gln Leu Phe His Ile Asp Phe Gly His Ile Leu Gly Asn
259      930                      935                      940
261 ttc aaa tct aag ttt ggc att aaa agg gag cga gtg cct ttt att ctt      2880
262 Phe Lys Ser Lys Phe Gly Ile Lys Arg Glu Arg Val Pro Phe Ile Leu
263 945                      950                      955                      960
265 acc tat gat ttc atc cat gtc att caa caa gga aaa aca gga aat aca      2928
266 Thr Tyr Asp Phe Ile His Val Ile Gln Gln Gly Lys Thr Gly Asn Thr
267      965                      970                      975
269 gaa aag ttt ggc cgg ttc cgc cag tgt tgt gag gat gca tat ctg att      2976
270 Glu Lys Phe Gly Arg Phe Arg Gln Cys Cys Glu Asp Ala Tyr Leu Ile
271      980                      985                      990
273 tta cga cgg cat ggg aat ctc ttc atc act ctc ttt gcg ctg atg ttg      3024
274 Leu Arg Arg His Gly Asn Leu Phe Ile Thr Leu Phe Ala Leu Met Leu
275      995                      1000                      1005
277 act gca ggg ctt cct gaa ctc aca tca gtc aaa gat ata cag tat ctt      3072
278 Thr Ala Gly Leu Pro Glu Leu Thr Ser Val Lys Asp Ile Gln Tyr Leu
279      1010                      1015                      1020
281 aag gac tct ctt gca tta ggg aag agt gaa gaa gaa gca ctc aaa cag      3120
282 Lys Asp Ser Leu Ala Leu Gly Lys Ser Glu Glu Glu Ala Leu Lys Gln
283 1025                      1030                      1035                      1040
285 ttt aag caa aaa ttt gat gag gcg ctc agg gaa agc tgg act act aaa      3168
286 Phe Lys Gln Lys Phe Asp Glu Ala Leu Arg Glu Ser Trp Thr Thr Lys
287      1045                      1050                      1055
289 gtg aac tgg atg gcc cac aca gtt cgg aaa gac tac aga tct taa      3213
290 Val Asn Trp Met Ala His Thr Val Arg Lys Asp Tyr Arg Ser
291      1060                      1065                      1070
294 <210> SEQ ID NO: 2
295 <211> LENGTH: 21
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
W--> 299 <220> FEATURE:
299 <223> OTHER INFORMATION: PCR Primer
301 <400> SEQUENCE: 2
302 gcggtggatt cacagatagc a      21
305 <210> SEQ ID NO: 3
306 <211> LENGTH: 21
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
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311 <223> OTHER INFORMATION: PCR Primer
313 <400> SEQUENCE: 3
314 tggtagcttc ccgaggtacc t      21
317 <210> SEQ ID NO: 4
318 <211> LENGTH: 24
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
W--> 322 <220> FEATURE:
322 <223> OTHER INFORMATION: PCR Probe
324 <400> SEQUENCE: 4
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VERIFICATION SUMMARY  
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:299 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:311 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:322 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:333 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:344 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:355 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:366 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:378 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:389 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:400 M:258 W: Mandatory Feature missing, <220> FEATURE:  
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L:433 M:258 W: Mandatory Feature missing, <220> FEATURE:  
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